SEQUENCE LISTING

<110> Green, Allan
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        Stymne, Sten

<120>   FATTY ACID EPOXYGENASE GENES FROM PLANTS AND USES THEREFOR IN
MODIFYING FATTY ACID METABOLISM

<130>   26-98A

<150>   US 09/059769

<151>   1998-04-14

<150>   US 60/043706

<151>   1997-04-16

<150>   AU PO6223

<151>   1997-04-15

<150>   AU PO6226

<151>   1997-04-15

<150>   US 60/050403

<151>   1997-06-20

<160>   24

<170>   PatentIn version 3.1

<210> 1

<211> 1358

<212> DNA

<213> Crepis palaestina

<220>

<221> CDS

<222> (30)..(1151)

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                                   Met Gly Ala Gly Gly Arg Gly Arg
                                   1               5

aca tcg gaa aaa tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc     101
Thr Ser Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr
    10              15                  20

ttc tca ctg agt gaa ttg aag caa gca atc cct ccc cat tgc ttc cag     149
Phe Ser Leu Ser Glu Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln
25              30                  35                      40

aga tct gta atc cgc tca tct tac tat gtt gtt caa gat ctc att att     197
Arg Ser Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile
                45              50                  55

gcc tac atc ttc tac ttc ctt gcc aac aca tat atc cct act ctt cct     245
Ala Tyr Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Thr Leu Pro
                60              65                  70

act agt cta gcc tac tta gct tgg ccc gtt tac tgg ttc tgt caa gct     293
Thr Ser Leu Ala Tyr Leu Ala Trp Pro Val Tyr Trp Phe Cys Gln Ala
        75              80                  85

agc gtc ctc act ggc tta tgg atc ctc ggc cac gaa tgt ggt cac cat     341
Ser Val Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His
        90              95                  100

gcc ttt agc aac tac aca tgg ttt gac gac act gtg ggc ttc atc ctc     389
Ala Phe Ser Asn Tyr Thr Trp Phe Asp Asp Thr Val Gly Phe Ile Leu
105              110                 115                     120

cac tca ttt ctc ctc acc ccg tat ttc tct tgg aaa ttc agt cac cgg     437
His Ser Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Phe Ser His Arg
                125                 130                 135
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aat cac cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att          485
Asn His His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile
            140                 145                 150


ccg aaa agc aag tcc aaa ctc gcg cgt atc tat aaa ctt ctt aac aac          533
Pro Lys Ser Lys Ser Lys Leu Ala Arg Ile Tyr Lys Leu Leu Asn Asn
            155                 160                 165


cca cct ggt cgg ctg ttg gtt ttg att atc atg ttc acc cta gga ttt          581
Pro Pro Gly Arg Leu Leu Val Leu Ile Ile Met Phe Thr Leu Gly Phe
        170                 175                 180


cct tta tac ctc ttg aca aat att tcc ggc aag aaa tac gac agg ttt          629
Pro Leu Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe
185                 190                 195                 200


gcc aac cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg          677
Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg
            205                 210                 215


ttt cag gtc ttc ctt tcg gat ctt ggt ctt ctt gcc gtg ttt tat gga         725
Phe Gln Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly
            220                 225                 230


att aaa gtt gct gta gca aat aaa gga gct gct tgg gta gcg tgc atg          773
Ile Lys Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met
            235                 240                 245


tat gga gtt ccg gta tta ggc gta ttt acc ttt ttc gat gtg atc acc          821
Tyr Gly Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr
            250                 255                 260


ttc ttg cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa          869
Phe Leu His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu
265                 270                 275                 280


tgg aac tgg atc aga ggg gcc ttg tca gca atc gat agg gac ttt gga          917
Trp Asn Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Arg Asp Phe Gly
                285                 290                 295


ttc ctg aat agt gtt ttc cat gat gtt aca cac act cat gtc atg cat          965
Phe Leu Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His
                300                 305                 310


cat ttg ttt tca tac att cca cac tat cat gca aag gag gca agg gat         1013
His Leu Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp
            315                 320                 325


gca atc aag cca atc ttg ggc gac ttt tat atg atc gac agg act cca         1061
Ala Ile Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro
            330                 335                 340


att tta aaa gca atg tgg aga gag ggc agg gag tgc atg tac atc gag         1109
Ile Leu Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu
345                 350                 355                 360
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```
cct gat agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg        1151
Pro Asp Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
            365                     370

tgatcatatg caaaatgcac atgcattttc aaaccctcta gttacgtttg ttctatgtat  1211

aataaaccgc cggtcctttg gttgactatg cctaagccag gcgaaacagt taaataatat  1271

cggtatgatg tgtaatgaaa gtatgtggtt gtctggtttt gttgctatga aagaaagtat  1331

gtggttgtcg gtcaaaaaaa aaaaaaa                                     1358
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<210> 2

<211> 374

<212> PRT

<213> Crepis palaestina

<400> 2

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1               5                   10                  15


Arg Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Glu Leu Lys Gln
            20                  25                  30


Ala Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr
            35                  40                  45


Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala
        50                  55                  60


Asn Thr Tyr Ile Pro Thr Leu Pro Thr Ser Leu Ala Tyr Leu Ala Trp
65                  70                  75                  80


Pro Val Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile
                85                  90                  95


Leu Gly His Glu Cys Gly His His Ala Phe Ser Asn Tyr Thr Trp Phe
            100                 105                 110


Asp Asp Thr Val Gly Phe Ile Leu His Ser Phe Leu Leu Thr Pro Tyr
            115                 120                 125
```

Phe Ser Trp Lys Phe Ser His Arg Asn His His Ser Asn Thr Ser Ser
    130   135   140

Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Ala
145   150   155   160

Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu
                165   170   175

Ile Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile
            180   185   190

Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser
        195   200   205

Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu
    210   215   220

Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys
225   230   235   240

Gly Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val
            245   250   255

Phe Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser
            260   265   270

Ser Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu
        275   280   285

Ser Ala Ile Asp Arg Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp
    290   295   300

Val Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His
305   310   315   320

Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp
            325   330   335

Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu
            340   345   350

Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val
        355   360   365

Tyr Trp Tyr His Lys Leu
    370

<210> 3

<211> 1309

<212> DNA

<213> Crepis sp.

<220>

<221> misc_feature

<222> (937)..(937)

<223> N is any nucleotide residue

<220>

<221> CDS

<222> (26)..(1147)

<223>

<220>

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<222> (901)..(901)

<223> N is any nucleotide residue

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tgttgaccat aaatcatcta tcaac atg ggt gcc ggc ggc cgt ggt cgg tcg   52
                             Met Gly Ala Gly Gly Arg Gly Arg Ser
                             1   5

gaa aag tcg gtc atg gaa cgt gtc tca gtt gat cca gta acc ttc tca   100
Glu Lys Ser Val Met Glu Arg Val Ser Val Asp Pro Val Thr Phe Ser
10   15   20   25

ctg agt gat ttg aag caa gca atc cct cca cat tgc ttc cag cga tct   148
Leu Ser Asp Leu Lys Gln Ala Ile Pro Pro His Cys Phe Gln Arg Ser
                30   35   40

```
gtc atc cgt tca tct tat tac gtt gtt cag gat ctc ata att gcc tac       196
Val Ile Arg Ser Ser Tyr Tyr Val Val Gln Asp Leu Ile Ile Ala Tyr
            45              50                  55

atc ttc tac ttc ctt gcc aac aca tat atc cct aat ctc cct cat cct       244
Ile Phe Tyr Phe Leu Ala Asn Thr Tyr Ile Pro Asn Leu Pro His Pro
            60              65                  70

cta gcc tac tta gct tgg ccg ctt tac tgg ttc tgt caa gct agc gtc       292
Leu Ala Tyr Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Ala Ser Val
        75              80                  85

ctc act ggg tta tgg atc ctc ggc cat gaa tgt ggt cac cat gcc tat       340
Leu Thr Gly Leu Trp Ile Leu Gly His Glu Cys Gly His His Ala Tyr
90              95                  100                 105

agc aac tac aca tgg gtt gac gac act gtg ggc ttc atc atc cat tca       388
Ser Asn Tyr Thr Trp Val Asp Asp Thr Val Gly Phe Ile Ile His Ser
            110                 115                 120

ttt ctc ctc acc ccg tat ttc tct tgg aaa tac agt cac cgg aat cac       436
Phe Leu Leu Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His
            125                 130                 135

cat tcc aac aca agt tcg att gat aac gat gaa gtt tac att ccg aaa       484
His Ser Asn Thr Ser Ser Ile Asp Asn Asp Glu Val Tyr Ile Pro Lys
            140                 145                 150

agc aag tcc aaa ctc aag cgt atc tat aaa ctt ctt aac aac cca cct       532
Ser Lys Ser Lys Leu Lys Arg Ile Tyr Lys Leu Leu Asn Asn Pro Pro
        155                 160                 165

ggt cga ctg ttg gtt ttg gtt atc atg ttc acc cta gga ttt cct tta       580
Gly Arg Leu Leu Val Leu Val Ile Met Phe Thr Leu Gly Phe Pro Leu
170                 175                 180                 185

tac ctc ttg aca aat att tcc ggc aag aaa tac gat agg ttt gcc aac       628
Tyr Leu Leu Thr Asn Ile Ser Gly Lys Lys Tyr Asp Arg Phe Ala Asn
            190                 195                 200

cac ttc gac ccc atg agt cca att ttc aaa gaa cgt gag cgg ttt cag       676
His Phe Asp Pro Met Ser Pro Ile Phe Lys Glu Arg Glu Arg Phe Gln
            205                 210                 215

gtc ttc ctt tcg gat ctt ggt ctt ctt gct gtg ttt tat gga att aaa       724
Val Phe Leu Ser Asp Leu Gly Leu Leu Ala Val Phe Tyr Gly Ile Lys
            220                 225                 230

gtt gct gta gca aat aaa gga gct gct tgg gtg gcg tgc atg tat gga       772
Val Ala Val Ala Asn Lys Gly Ala Ala Trp Val Ala Cys Met Tyr Gly
        235                 240                 245

gtt ccg gtg cta ggc gta ttt acc ttt ttc gat gtg atc acg ttc tta       820
Val Pro Val Leu Gly Val Phe Thr Phe Phe Asp Val Ile Thr Phe Leu
250                 255                 260                 265
```

```
cac cac acc cat cag tcg tcg cct cat tat gat tca act gaa tgg aac       868
His His Thr His Gln Ser Ser Pro His Tyr Asp Ser Thr Glu Trp Asn
            270             275                 280

tgg atc aga ggg gct ttg tca gca atc gat agn gac ttt ggg ttc ctg       916
Trp Ile Arg Gly Ala Leu Ser Ala Ile Asp Xaa Asp Phe Gly Phe Leu
            285             290                 295

aat agt gtt ttc cat gat gtn aca cac act cac gtc atg cat cat ttg       964
Asn Ser Val Phe His Asp Val Thr His Thr His Val Met His His Leu
            300             305                 310

ttt tca tac att cca cac tat cat gca aag gaa gca agg gat gca atc      1012
Phe Ser Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile
            315             320                 325

aaa ccg atc ttg ggc gac ttt tat atg atc gat agg act cca att tta      1060
Lys Pro Ile Leu Gly Asp Phe Tyr Met Ile Asp Arg Thr Pro Ile Leu
330             335             340                 345

aaa gca atg tgg aga gag ggc agg gaa tgc atg tac atc gag cct gat      1108
Lys Ala Met Trp Arg Glu Gly Arg Glu Cys Met Tyr Ile Glu Pro Asp
            350             355                 360

agc aag ctc aaa ggt gtt tat tgg tat cat aaa ttg tga tcatatgcaa      1157
Ser Lys Leu Lys Gly Val Tyr Trp Tyr His Lys Leu
            365             370

aatgcacatg cattttcaaa ccctctagtt acctttgttc tatgtataat aagaccgccg   1217

gtcctatggt tttctatgcc taagccaggc gaaatagtta ataatatcg gtatgatgta   1277

atgaaagtat gtggttgtct aaaaaaaaaa aa                                 1309
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<210> 4

<211> 373

<212> PRT

<213> Crepis sp.

<220>

<221> misc_feature

<222> (292)..(292)

<223> The 'Xaa' at location 292 stands for Arg, or Ser.

<220>

<221> misc_feature

<222> (937)..(937)

<223> N is any nucleotide residue

<220>

<221> misc_feature

<222> (901)..(901)

<223> N is any nucleotide residue

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1               5                   10                  15

Val Ser Val Asp Pro Val Thr Phe Ser Leu Ser Asp Leu Lys Gln Ala
            20                  25                  30

Ile Pro Pro His Cys Phe Gln Arg Ser Val Ile Arg Ser Ser Tyr Tyr
        35                  40                  45

Val Val Gln Asp Leu Ile Ile Ala Tyr Ile Phe Tyr Phe Leu Ala Asn
        50                  55                  60

Thr Tyr Ile Pro Asn Leu Pro His Pro Leu Ala Tyr Leu Ala Trp Pro
65                  70                  75                  80

Leu Tyr Trp Phe Cys Gln Ala Ser Val Leu Thr Gly Leu Trp Ile Leu
                85                  90                  95

Gly His Glu Cys Gly His His Ala Tyr Ser Asn Tyr Thr Trp Val Asp
                100                 105                 110

Asp Thr Val Gly Phe Ile Ile His Ser Phe Leu Leu Thr Pro Tyr Phe
            115                 120                 125

Ser Trp Lys Tyr Ser His Arg Asn His His Ser Asn Thr Ser Ser Ile
        130                 135                 140

Asp Asn Asp Glu Val Tyr Ile Pro Lys Ser Lys Ser Lys Leu Lys Arg
145                 150                 155                 160

Ile Tyr Lys Leu Leu Asn Asn Pro Pro Gly Arg Leu Leu Val Leu Val
                165                 170                 175
```

Ile Met Phe Thr Leu Gly Phe Pro Leu Tyr Leu Leu Thr Asn Ile Ser
                180   185   190

Gly Lys Lys Tyr Asp Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro
            195   200   205

Ile Phe Lys Glu Arg Glu Arg Phe Gln Val Phe Leu Ser Asp Leu Gly
        210   215   220

Leu Leu Ala Val Phe Tyr Gly Ile Lys Val Ala Val Ala Asn Lys Gly
225   230   235   240

Ala Ala Trp Val Ala Cys Met Tyr Gly Val Pro Val Leu Gly Val Phe
                245   250   255

Thr Phe Phe Asp Val Ile Thr Phe Leu His His Thr His Gln Ser Ser
            260   265   270

Pro His Tyr Asp Ser Thr Glu Trp Asn Trp Ile Arg Gly Ala Leu Ser
            275   280   285

Ala Ile Asp Xaa Asp Phe Gly Phe Leu Asn Ser Val Phe His Asp Val
        290   295   300

Thr His Thr His Val Met His His Leu Phe Ser Tyr Ile Pro His Tyr
305   310   315   320

His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Ile Leu Gly Asp Phe
                325   330   335

Tyr Met Ile Asp Arg Thr Pro Ile Leu Lys Ala Met Trp Arg Glu Gly
            340   345   350

Arg Glu Cys Met Tyr Ile Glu Pro Asp Ser Lys Leu Lys Gly Val Tyr
            355   360   365

Trp Tyr His Lys Leu
        370

<210>   5

<211>   550

<212> DNA

<213> Vernonia galamensis

<220>

<221> CDS

<222> (1)..(549)

<223>

<400> 5

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His His Ala Phe Ser Asp Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe
1               5                   10                  15

atc ctt cac ttt gca ctc ttc acc cct tat ttc tct tgg aaa tac agt        96
Ile Leu His Phe Ala Leu Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser
            20                  25                  30

cac cgt aat cac cat gcc aac aca aac tct ctt gta acc gat gaa gta       144
His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val
        35                  40                  45

tac atc cct aaa gtt aaa tcc aag gtc aag att tat tcc aaa atc ctt       192
Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu
        50                  55                  60

aac aac cct cct ggt cgc gtt ttc acc ttg gct ttc aga ttg atc gtg       240
Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val
65                  70                  75                  80

ggt ttt cct tta tac ctt ttc acc aat gtt tca ggc aag aaa tac gaa       288
Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu
                85                  90                  95

cgt ttt gcc aac cat ttt gat ccc atg agt ccc att ttc acc gag cgt       336
Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg
            100                 105                 110

gag cat gta caa gtc ttg ctt tct gat ttt ggt ctc ata gca gtt gct       384
Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala
            115                 120                 125

tac gtg gtt cgt caa gct gta ctg gct aaa gga ggt gct tgg gtg atg       432
Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met
        130                 135                 140

tgc att tac gga gtt cct gtg ctg gcc gta aac gca ttc ttt gtt tta       480
Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu
145                 150                 155                 160
```

```
atc act tat ctt cac cac acg cat ctc tca ctg ccc cac tat gat agc      528
Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
                165                     170                 175

tca gaa tgg gac tgg cta cga g                                        550
Ser Glu Trp Asp Trp Leu Arg
                180
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<210> 6

<211> 183

<212> PRT

<213> Vernonia galamensis

<400> 6

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His His Ala Phe Ser Asp Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe
1               5                   10                  15


Ile Leu His Phe Ala Leu Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser
            20                  25                  30


His Arg Asn His His Ala Asn Thr Asn Ser Leu Val Thr Asp Glu Val
            35                  40                  45


Tyr Ile Pro Lys Val Lys Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu
    50                  55                  60


Asn Asn Pro Pro Gly Arg Val Phe Thr Leu Ala Phe Arg Leu Ile Val
65                  70                  75                  80


Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu
                85                  90                  95


Arg Phe Ala Asn His Phe Asp Pro Met Ser Pro Ile Phe Thr Glu Arg
                100                 105                 110


Glu His Val Gln Val Leu Leu Ser Asp Phe Gly Leu Ile Ala Val Ala
        115                 120                 125


Tyr Val Val Arg Gln Ala Val Leu Ala Lys Gly Gly Ala Trp Val Met
    130                 135                 140


Cys Ile Tyr Gly Val Pro Val Leu Ala Val Asn Ala Phe Phe Val Leu
145                 150                 155                 160
```

```
Ile Thr Tyr Leu His His Thr His Leu Ser Leu Pro His Tyr Asp Ser
            165             170             175


Ser Glu Trp Asp Trp Leu Arg
            180
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<210> 7

<211> 177

<212> DNA

<213> Crepis alpina

<220>

<221> CDS

<222> (1)..(177)

<223>

<400> 7

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gaa tgc ggt cac cat gcc ttc agc gac tac cag tgg gtt gac gac aat    48
Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Asn
1               5               10              15

gtg ggc ttc atc ctc cac tcg ttt ctc atg acc ccg tat ttc tcc tgg    96
Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe Ser Trp
                20              25              30

aaa tac agc cac cgg aac cac cat gcc aac aca aat tcg ctt gac aac   144
Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn
            35              40              45

gat gaa gtt tac atc ccc aaa agc aag gcc aaa                       177
Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys
        50              55
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<210> 8

<211> 59

<212> PRT

<213> Crepis alpina

<400> 8

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Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Val Asp Asp Asn
1               5               10              15
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Val Gly Phe Ile Leu His Ser Phe Leu Met Thr Pro Tyr Phe Ser Trp
            20   25   30

Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser Leu Asp Asn
        35   40   45

Asp Glu Val Tyr Ile Pro Lys Ser Lys Ala Lys
        50   55

<210> 9

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 9

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
1   5   10   15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
            20   25   30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
        35   40   45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
        50   55   60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65   70   75   80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                85   90   95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
            100   105   110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
        115   120   125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165   170   175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
                180   185   190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
        195   200   205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
        210   215   220

Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
225   230   235   240

Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
                245   250   255

Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
                260   265   270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
        275   280   285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
        290   295   300

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
305   310   315   320

Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
                325   330   335

Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
                340   345   350

Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
     355   360   365

Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
     370   375   380

<210> 10

<211> 384

<212> PRT

<213> Brassica juncea

<400> 10

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Ser Pro Lys Lys Ser
1   5   10   15

Glu Thr Asp Thr Leu Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
       20   25   30

Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
       35   40   45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Val Ala Ser
     50   55   60

Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
65   70   75   80

Leu Ser Tyr Val Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Val Val
          85   90   95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
       100   105   110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
       115   120   125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
       130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
            165   .   170   175

Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
            180   185   190

Tyr Trp Ala Phe Asn Val Ser Gly Arg Pro Tyr Pro Glu Gly Phe Ala
        195   200   205

Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
    210   215   220

Gln Ile Tyr Val Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
225   230   235   240

Tyr Arg Tyr Ala Ala Ala Gln Gly Val Ala Ser Met Val Cys Leu Tyr
            245   250   255

Gly Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr
            260   265   270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
        275   280   285

Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
    290   295   300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
305   310   315   320

Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Val Thr Lys Ala
            325   330   335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp
            340   345   350

Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
            355   360   365

Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
    370   375   380

<210>   11

<211>   367

<212>   PRT

<213>   Glycine max

<400>   11

Met Gly Ala Gly Gly Arg Thr Asp Val Pro Pro Ala Asn Arg Lys Ser
1   5   10   15

Glu Val Asp Pro Leu Lys Arg Val Pro Phe Glu Lys Pro Gln Phe Ser
            20   25   30

Leu Ser Gln Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
            35   40   45

Val Leu Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe
        50   55   60

Cys Leu Tyr Tyr Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro
65   70   75   80

Leu Ser Phe Arg Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile
                85   90   95

Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
                100   105   110

Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly Leu Ile Leu His Ser
            115   120   125

Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
        130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Gly Arg Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu
                165   170   175

```
Tyr Leu Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
            180             185             190

His Tyr Asp Pro Tyr Gly Pro Ile Tyr Ser Asp Arg Glu Arg Leu Gln
            195             200             205

Ile Tyr Ile Ser Asp Ala Gly Val Leu Ala Val Val Tyr Gly Leu Phe
    210             215             220

Arg Leu Ala Met Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly
225             230             235             240

Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Phe Leu
            245             250             255

Gln His Thr His Pro Ala Leu Pro His Tyr Thr Ser Ser Glu Trp Asp
            260             265             270

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
            275             280             285

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
    290             295             300

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
305             310             315             320

Lys Pro Ile Leu Gly Glu Tyr Tyr Arg Phe Asp Glu Thr Pro Phe Val
            325             330             335

Lys Ala Met Trp Arg Glu Ala Arg Glu Cys Ile Tyr Val Glu Pro Asp
            340             345             350

Gln Ser Thr Glu Ser Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
            355             360             365
```

<210> 12

<211> 383

<212> PRT

<213> Solanum commersonii

<400> 12

Met Gly Ala Gly Gly Arg Met Ser Ala Pro Asn Gly Glu Thr Glu Val
1   5   10   15

Lys Arg Asn Pro Leu Gln Lys Val Pro Thr Ser Lys Pro Pro Phe Thr
            20   25   30

Val Gly Asp Ile Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser
        35   40   45

Leu Ile Arg Ser Phe Ser Tyr Val Val Tyr Asp Leu Ile Leu Val Ser
    50   55   60

Ile Met Tyr Tyr Val Ala Asn Thr Tyr Phe His Leu Leu Pro Ser Pro
65   70   75   80

Tyr Cys Tyr Ile Ala Trp Pro Ile Tyr Trp Ile Cys Gln Gly Cys Val
            85   90   95

Cys Thr Gly Ile Trp Val Asn Ala His Glu Cys Gly His His Ala Phe
            100   105   110

Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Leu Ile Leu His Ser
        115   120   125

Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
    130   135   140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145   150   155   160

Pro Lys Ser Gln Leu Gly Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro
            165   170   175

Gly Arg Val Leu Ser Leu Thr Ile Thr Leu Thr Leu Gly Trp Pro Leu
            180   185   190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys
        195   200   205

His Tyr Asp Pro Tyr Gly Pro Ile Tyr Asn Asn Arg Glu Arg Leu Gln
    210   215   220

```
Ile Phe Ile Ser Asp Ala Gly Val Leu Gly Val Cys Tyr Leu Leu Tyr
225             230             235                 240


Arg Ile Ala Leu Val Lys Gly Leu Ala Trp Leu Val Cys Val Tyr Gly
            245             250                 255


Val Pro Leu Leu Val Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
            260             265             270


Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp
        275             280             285


Trp Leu Arg Gly Ala Leu Ala Thr Cys Asp Arg Asp Tyr Gly Val Leu
    290             295             300


Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Val His His Leu
305             310             315                 320


Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Val
            325             330             335


Lys Pro Leu Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Ile Tyr
            340             345             350


Lys Glu Met Trp Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Lys Asp
        355             360             365


Glu Ser Ser Gln Gly Lys Gly Val Phe Trp Tyr Lys Asn Lys Leu
370             375             380


<210> 13

<211> 387

<212> PRT

<213> Glycine max


<400> 13

Met Gly Leu Ala Lys Glu Thr Thr Met Gly Gly Arg Gly Arg Val Ala
1               5               10                  15
```

Lys Val Glu Val Gln Gly Lys Lys Pro Leu Ser Arg Val Pro Asn Thr
        20   25   30

Lys Pro Pro Phe Thr Val Gly Gln Leu Lys Lys Ala Ile Pro Pro His
        35   40   45

Cys Phe Gln Arg Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp
    50   55   60

Leu Ser Phe Ala Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu
65   70   75   80

Leu Pro Gln Pro Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu
            85   90   95

Gln Gly Cys Leu Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly
        100   105   110

His His Ala Phe Ser Lys Tyr Gln Trp Val Asp Asp Val Val Gly Leu
        115   120   125

Thr Leu His Ser Thr Leu Leu Val Pro Tyr Phe Ser Trp Lys Ile Ser
    130   135   140

His Arg Arg His His Ser Asn Thr Gly Ser Leu Asp Arg Asp Glu Val
145   150   155   160

Phe Val Pro Lys Pro Lys Ser Lys Val Ala Trp Phe Ser Lys Tyr Leu
            165   170   175

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
            180   185   190

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
        195   200   205

Ser Phe Ala Ser His Tyr His Pro Tyr Ala Pro Ile Tyr Ser Asn Arg
        210   215   220

Glu Arg Leu Leu Ile Tyr Val Ser Asp Val Ala Leu Phe Ser Val Thr
225   230   235   240

Tyr Ser Leu Tyr Arg Val Ala Thr Leu Lys Gly Leu Val Trp Leu Leu
                245   250   255

Cys Val Tyr Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Thr
            260   265   270

Ile Thr Tyr Leu Gln His Thr His Phe Ala Leu Pro His Tyr Asp Ser
        275   280   285

Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr Met Asp Arg Asp
    290   295   300

Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr Asp Thr His Val
305   310   315   320

Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala
            325   330   335

Thr Asn Ala Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp
            340   345   350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr
        355   360   365

Val Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg
    370   375   380

Asn Lys Tyr
385

<210> 14

<211> 387

<212> PRT

<213> Ricinus communis

<400> 14

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
1   5   10   15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
            20   25   30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
     35   40   45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
     50   55   60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
65   70   75   80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
            85   90   95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
          100   105   110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
        115   120   125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
    130   135   140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
145   150   155   160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
          165   170   175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
        180   185   190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
    195   200   205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
210   215   220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225   230   235   240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
        245   250   255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
            260   265   270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
        275   280   285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
    290   295   300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
305   310   315   320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
            325   330   335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
            340   345   350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
            355   360   365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
    370   375   380

Asn Lys Tyr
385

<210> 15

<211> 6

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 15

His Glu Cys Gly His His
1   5

<210> 16

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 16

His Arg Asn His His
1   5

<210> 17

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 17

His Val Met His His
1   5

<210> 18

<211> 5

<212> PRT

<213> mixed function monooxygenase peptide motif

<400> 18

His Val Leu His His
1   5

<210> 19

<211> 1199

<212> DNA

<213> Vernonia galamensis

<220>

<221> CDS

<222> (44)..(1195)

<223>

<400> 19

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tattacacat ttacactgat ctgttaatca aatttcaaac aaa atg gga gct ggt          55
                                                   Met Gly Ala Gly
                                                   1


ggc cga atg aat acc acc gat gat gat cag aag aat ctc ttc caa cgc         103
Gly Arg Met Asn Thr Thr Asp Asp Asp Gln Lys Asn Leu Phe Gln Arg
5                   10              15                  20


gta cca gcc tcc aaa cca cca ttc tcc ttg gct gat ctt aag aaa gcc        151
Val Pro Ala Ser Lys Pro Pro Phe Ser Leu Ala Asp Leu Lys Lys Ala
                25              30                  35


ata cca ccc cac tgt ttc caa aga tcc ctc ctc cgt tca tct tac tat        199
Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Arg Ser Ser Tyr Tyr
            40              45              50


gtg gtt cat gat ctc gtc gta gcc tac gtc ttt tac tat ctc gcc aac        247
Val Val His Asp Leu Val Val Ala Tyr Val Phe Tyr Tyr Leu Ala Asn
        55              60              65


aca tac atc cct ctt ctt ccc tcc cct ctt gcc tac tta tta gct tgg        295
Thr Tyr Ile Pro Leu Leu Pro Ser Pro Leu Ala Tyr Leu Leu Ala Trp
    70              75              80


ccc ctt tac tgg ttc tgt cag ggt agc atc ctc acc ggt gtc tgg gtc        343
Pro Leu Tyr Trp Phe Cys Gln Gly Ser Ile Leu Thr Gly Val Trp Val
85              90              95                  100


atc ggt cat gaa tgt ggc cac cat gcc ttc agt gac tat caa tgg ata        391
Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp Tyr Gln Trp Ile
            105             110             115


gac gac act gtg ggc ttc atc ctt cac tct gca ctc ttc acc cct tat        439
Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu Phe Thr Pro Tyr
        120             125             130


ttc tct tgg aaa tac agt cac cgt aat cac cat gcc aac aca aac tct        487
Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala Asn Thr Asn Ser
        135             140             145


ctt gat aac gat gaa gta tac atc cct aaa gtt aaa tcc aag gtc aag        535
Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Val Lys Ser Lys Val Lys
    150             155             160


att tat tcc aaa atc ctt aac aac cct cct ggt cgc gtt ttc acc ttg        583
Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg Val Phe Thr Leu
165             170             175             180


gct ttc aga ttg atc gtg ggt ttt cct tta tac ctt ttc acc aat gtt        631
Ala Phe Arg Leu Ile Val Gly Phe Pro Leu Tyr Leu Phe Thr Asn Val
            185             190             195


tca ggc aag aaa tac gaa cgt ttt gcc aac cat ttt gat ccc atg agt        679
Ser Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe Asp Pro Met Ser
            200             205             210
```

```
ccc att ttc acc gag cgt gag cat gta caa gtc ttg ctt tct gat ttt        727
Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu Leu Ser Asp Phe
        215                 220                 225

ggt ctc ata gca gtt gct tac gtg gtt cgt caa gct gta ctg gct aaa        775
Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala Val Leu Ala Lys
        230                 235                 240

gga ggt gct tgg gtg atg tgc att tac gga gtt cct gtg ctg gcc gta        823
Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro Val Leu Ala Val
245                 250                 255                 260

aac gca ttc ttt gtt tta atc act tat ctt cac cac acg cat ctc tca        871
Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His Thr His Leu Ser
                265                 270                 275

ctg cct cac tat gat tcg act gaa tgg gac tgg atc aag gga gct ttg        919
Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile Lys Gly Ala Leu
                280                 285                 290

tgc acc atc gac aga gat ttc gga ttc ttg aat agg gtt ttc cac gac        967
Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg Val Phe His Asp
                295                 300                 305

gtg aca cac acc cat gtg ttg cat cat ttg ata tcg tac att cct cat       1015
Val Thr His Thr His Val Leu His His Leu Ile Ser Tyr Ile Pro His
                310                 315                 320

tat cat gca aag gag gca aga gac gcc atc aaa ccg gtg ttg ggc gaa       1063
Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro Val Leu Gly Glu
325                 330                 335                 340

tac tat aag atc gac agg aca ccg atc gtg aag gca atg tgg agg gaa       1111
Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala Met Trp Arg Glu
                345                 350                 355

gca aag aat gca tat aca ttg agg ctg atg aag ata gcg agc acc aag       1159
Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile Ala Ser Thr Lys
                360                 365                 370

gca cat act ggt acc aca agt tgt aaa gcc aga tcc taag                  1199
Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
                375                 380
```

<210> 20

<211> 384

<212> PRT

<213> Vernonia galamensis

<400> 20

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Met Gly Ala Gly Gly Arg Met Asn Thr Thr Asp Asp Asp Gln Lys Asn
1               5               10                  15


Leu Phe Gln Arg Val Pro Ala Ser Lys Pro Pro Phe Ser Leu Ala Asp
            20              25                  30


Leu Lys Lys Ala Ile Pro Pro His Cys Phe Gln Arg Ser Leu Leu Arg
        35              40              45


Ser Ser Tyr Tyr Val Val His Asp Leu Val Val Ala Tyr Val Phe Tyr
        50              55                  60


Tyr Leu Ala Asn Thr Tyr Ile Pro Leu Leu Pro Ser Pro Leu Ala Tyr
65              70              75                  80


Leu Leu Ala Trp Pro Leu Tyr Trp Phe Cys Gln Gly Ser Ile Leu Thr
                85              90                  95


Gly Val Trp Val Ile Gly His Glu Cys Gly His His Ala Phe Ser Asp
                100             105             110


Tyr Gln Trp Ile Asp Asp Thr Val Gly Phe Ile Leu His Ser Ala Leu
            115             120             125


Phe Thr Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Asn His His Ala
    130             135             140


Asn Thr Asn Ser Leu Asp Asn Asp Glu Val Tyr Ile Pro Lys Val Lys
145             150             155                 160


Ser Lys Val Lys Ile Tyr Ser Lys Ile Leu Asn Asn Pro Pro Gly Arg
                165             170             175


Val Phe Thr Leu Ala Phe Arg Leu Ile Val Gly Phe Pro Leu Tyr Leu
                180             185             190


Phe Thr Asn Val Ser Gly Lys Lys Tyr Glu Arg Phe Ala Asn His Phe
    195             200             205


Asp Pro Met Ser Pro Ile Phe Thr Glu Arg Glu His Val Gln Val Leu
    210             215             220
```

Leu Ser Asp Phe Gly Leu Ile Ala Val Ala Tyr Val Val Arg Gln Ala
225   230   235   240

Val Leu Ala Lys Gly Gly Ala Trp Val Met Cys Ile Tyr Gly Val Pro
                245   250   255

Val Leu Ala Val Asn Ala Phe Phe Val Leu Ile Thr Tyr Leu His His
            260   265   270

Thr His Leu Ser Leu Pro His Tyr Asp Ser Thr Glu Trp Asp Trp Ile
            275   280   285

Lys Gly Ala Leu Cys Thr Ile Asp Arg Asp Phe Gly Phe Leu Asn Arg
    290   295   300

Val Phe His Asp Val Thr His Thr His Val Leu His His Leu Ile Ser
305   310   315   320

Tyr Ile Pro His Tyr His Ala Lys Glu Ala Arg Asp Ala Ile Lys Pro
            325   330   335

Val Leu Gly Glu Tyr Tyr Lys Ile Asp Arg Thr Pro Ile Val Lys Ala
            340   345   350

Met Trp Arg Glu Ala Lys Asn Ala Tyr Thr Leu Arg Leu Met Lys Ile
    355   360   365

Ala Ser Thr Lys Ala His Thr Gly Thr Thr Ser Cys Lys Ala Arg Ser
    370   375   380

<210>   21

<211>   5

<212>   PRT

<213>   mixed function monooxygenase consensus motif

<220>

<221>   MISC_FEATURE

<222>   (2)..(4)

<223>   Xaa at position 2 is any amino acid; Xaa at position 3 is any amino acid; Xaa at position 4 is any amino acid;

<400> 21

His Xaa Xaa Xaa His
1   5

<210> 22

<211> 6

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(5)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
      no acid; Xaa at position 4 is any amino acid;Xaa at position 5 is
       any amino acid;

<400> 22

His Xaa Xaa Xaa Xaa His
1   5

<210> 23

<211> 5

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(3)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
      no acid;

<400> 23

His Xaa Xaa His His
1   5

<210> 24

<211> 6

<212> PRT

<213> mixed function monooxygenase consensus motif

<220>

<221> MISC_FEATURE

<222> (2)..(4)

<223> Xaa at position 2 is any amino acid; Xaa at position 3 is any ami
no acid; Xaa at position 4 is any amino acid;

<400> 24

His Xaa Xaa Xaa His His
1   5